

1636

RAW SEQUENCE LISTING
 PATENT APPLICATION: US/09/641,892

DATE: 11/13/2000
 TIME: 11:03:57

Input Set : A:\ES.txt
 Output Set: N:\CRF3\11132000\I641892.raw

ENTERED

3 <110> APPLICANT: IZUI, HIROSHI
 4 MORIYA, MIKA
 5 HIRANO, SEIKO
 6 HARA, YOSHIHIKO
 7 ITO, HISAO
 8 MATSUI, KAZUHIKO
 10 <120> TITLE OF INVENTION: METHOD FOR PRODUCING L-GLUTAMIC ACID BY FERMENTATION ACCOMPANIED BY
 11 PRECIPITATION
 13 <130> FILE REFERENCE: 195942US0
 15 <140> CURRENT APPLICATION NUMBER: 09/641,892
 16 <141> CURRENT FILING DATE: 2000-08-18
 18 <150> PRIOR APPLICATION NUMBER: JP2000-78771
 19 <151> PRIOR FILING DATE: 2000-03-21
 21 <150> PRIOR APPLICATION NUMBER: JP11-234806
 22 <151> PRIOR FILING DATE: 1999-08-20
 24 <160> NUMBER OF SEQ ID NOS: 7
 26 <170> SOFTWARE: PatentIn version 3.0
 28 <210> SEQ ID NO: 1
 29 <211> LENGTH: 4556
 30 <212> TYPE: DNA
 31 <213> ORGANISM: Enterobacter agglomerans
 33 <220> FEATURE:
 34 <221> NAME/KEY: CDS
 35 <222> LOCATION: (2)..(121)
 37 <220> FEATURE:
 38 <221> NAME/KEY: CDS
 39 <222> LOCATION: (322)..(3129)
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 42 <221> NAME/KEY: CDS
 43 <222> LOCATION: (3145)..(4368)
 45 <220> FEATURE:
 46 <221> NAME/KEY: CDS
 47 <222> LOCATION: (4437)..(4556)
 49 <400> SEQUENCE: 1
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 51 Ala Phe Ser Val Phe Arg Cys His Ser Ile Met Asn Cys Val Ser Val
 52 1 5 10 15
 54 tgt cct aaa ggg cta aac ccg acg cgc gct atc ggc cac att aag tcg 97
 55 Cys Pro Lys Gly Leu Asn Pro Thr Arg Ala Ile Gly His Ile Lys Ser
 56 20 25 30
 58 atg ctg ctg caa cgc agc gcg tag ttataccacc gggaaacctca ggttcccggt 151
 59 Met Leu Leu Gln Arg Ser Ala
 60 35
 62 attttacgga agcctctgta aacgggtccc caaccacgtt tacaaaaggtt cccttacggg 211
 64 ccggcgcgcg gctgcgcaca gtgctcgtat cgctgaactc actacggcaa accgcgaaag 271
 66 cggcaacaaa tgaaacctca aaaaagcata acattgctta agggatcaca atg cag 327
 67 Met Gln

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134	ggg	atg	gcg	cac	cgt	ggc	cgt	ctt	aac	gta	ctg	att	aac	gta	ctg	ggc	1143
135	Gly	Met	Ala	His	Arg	Gly	Arg	Leu	Asn	Val	Leu	Ile	Asn	Val	Leu	Gly	
136			300					305					310				
138	aaa	aag	cca	cag	gat	ctg	ttc	gac	gaa	ttc	tcc	ggt	aaa	cac	aaa	gag	1191
139	Lys	Lys	Pro	Gln	Asp	Leu	Phe	Asp	Glu	Phe	Ser	Gly	Lys	His	Lys	Glu	
140			315				320						325				
142	cat	ctg	ggc	acc	ggt	gat	gtg	aaq	tat	cac	atg	qgc	ttc	tct	tcg	gat	1239
143	His	Leu	Gly	Thr	Gly	Asp	Val	Lys	Tyr	His	Met	Gly	Phe	Ser	Ser	Asp	
144	330					335						340				345	
146	att	gaa	acc	gaa	ggt	ggt	ctg	gtg	cat	ctg	gcg	ctg	gcg	ttt	aac	ccg	1287
147	Ile	Glu	Thr	Glu	Gly	Gly	Leu	Val	His	Leu	Ala	Leu	Ala	Phe	Asn	Pro	
148				350						355					360		
150	tct	cac	ctg	gaa	att	gtc	agc	ccg	gtg	gtc	atg	qga	tcg	gta	cgt	gca	1335
151	Ser	His	Leu	Glu	Ile	Val	Ser	Pro	Val	Val	Met	Gly	Ser	Val	Arg	Ala	
152			365					370						375			
154	cgt	ctc	gat	cgt	ctg	gcc	gaa	ccg	gtc	agc	aat	aaa	gtg	ttg	cct	atc	1383
155	Arg	Leu	Asp	Arg	Leu	Ala	Glu	Pro	Val	Ser	Asn	Lys	Val	Leu	Pro	Ile	
156			380					385					390				
158	acc	att	cac	ggt	gat	gcg	gcg	gtg	att	ggt	cag	ggc	gtg	gtt	cag	gaa	1431
159	Thr	Ile	His	Gly	Asp	Ala	Ala	Val	Ile	Gly	Gln	Gly	Val	Val	Gln	Glu	
160			395				400					405					
162	acc	ctg	aac	atg	tct	cag	gcg	cgc	ggc	tac	gaa	gtg	ggc	ggc	acg	gta	1479
163	Thr	Leu	Asn	Met	Ser	Gln	Ala	Arg	Gly	Tyr	Glu	Val	Gly	Gly	Thr	Val	
164	410					415				420					425		
166	cgt	atc	gtc	att	aac	aac	cag	gtt	ggt	ttt	acc	acc	tcc	aac	ccg	aaa	1527
167	Arg	Ile	Val	Ile	Asn	Gln	Val	Gly	Phe	Thr	Thr	Ser	Asn	Pro	Lys		
168				430				435						440			
170	gat	gcg	cgt	tca	acc	ccg	tac	tgt	act	gac	atc	ggc	aag	atg	gtg	ctg	1575
171	Asp	Ala	Arg	Ser	Thr	Pro	Tyr	Cys	Thr	Asp	Ile	Gly	Lys	Met	Val	Leu	
172			445					450					455				
174	gca	ccg	att	ttc	cac	gtc	aat	gct	gac	gat	ccg	gaa	gcg	gtg	gcc	ttt	1623
175	Ala	Pro	Ile	Phe	His	Val	Asn	Ala	Asp	Asp	Pro	Glu	Ala	Val	Ala	Phe	
176			460					465				470					
178	gtt	acc	cgc	ctg	gcg	ctg	gac	tat	cgc	aac	acc	ttc	aaa	cgc	gat	gtg	1671
179	Val	Thr	Arg	Leu	Ala	Leu	Asp	Tyr	Arg	Asn	Thr	Phe	Lys	Arg	Asp	Val	
180			475				480					485					
182	ttt	atc	gat	ctg	gtg	tgc	tat	cgc	cgt	cat	ggt	cac	aac	gag	gcg	gat	1719
183	Phe	Ile	Asp	Leu	Val	Cys	Tyr	Arg	Arg	His	Gly	His	Asn	Glu	Ala	Asp	
184	490					495				500					505		
186	gag	cca	agt	gct	acc	cag	ccg	ttg	atg	tac	cag	aaa	atc	aaa	aag	cat	1767
187	Glu	Pro	Ser	Ala	Thr	Gln	Pro	Leu	Met	Tyr	Gln	Lys	Ile	Lys	Lys	His	
188				510				515						520			
190	ccg	acg	ccg	cgt	aaa	att	tac	gcc	gat	cgt	ctg	gaa	ggc	gaa	ggt	gtc	1815
191	Pro	Thr	Pro	Arg	Lys	Ile	Tyr	Ala	Asp	Arg	Leu	Glu	Gly	Glu	Gly	Val	
192				525				530						535			
194	gcg	tcg	cag	gaa	gat	gcc	acc	gag	atg	gtg	aac	ctg	tac	cgc	gat	gcg	1863
195	Ala	Ser	Gln	Glu	Asp	Ala	Thr	Glu	Met	Val	Asn	Leu	Tyr	Arg	Asp	Ala	
196			540					545						550			
198	ctc	gal	gcg	ggc	gaa	tgc	gtg	gtg	ccg	gaa	tgg	cgt	ccg	atg	agc	ctg	1911

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199	Leu	Asp	Ala	Gly	Glu	Cys	Val	Val	Pro	Glu	Trp	Arg	Pro	Met	Ser	Leu	
200		555					560					565					
202	cac	tcc	ttc	acg	tgg	tcg	cct	tat	ctg	aac	cac	gaa	tgg	gat	gag	cct	1959
203	His	Ser	Phe	Thr	Trp	Ser	Pro	Tyr	Leu	Asn	His	Glu	Trp	Asp	Glu	Pro	
204	570					575					580					585	
206	tat	ccg	gca	cag	gtt	gac	atg	aaa	cgc	ctg	aag	gaa	ctg	gca	ttg	cgt	2007
207	Tyr	Pro	Ala	Gln	Val	Asp	Met	Lys	Arg	Leu	Lys	Glu	Leu	Ala	Leu	Arg	
208					590					595					600		
210	atc	agc	cag	gtc	cct	gag	cag	att	gaa	gtg	cag	tcg	cgc	gtg	gcc	aag	2055
211	Ile	Ser	Gln	Val	Pro	Glu	Gln	Ile	Glu	Val	Gln	Ser	Arg	Val	Ala	Lys	
212				605					610					615			
214	atc	tat	aac	gat	cgc	aag	ctg	atg	gcc	gaa	ggc	gag	aaa	gcg	ttc	gac	2103
215	Ile	Tyr	Asn	Asp	Arg	Lys	Leu	Met	Ala	Glu	Gly	Glu	Lys	Ala	Phe	Asp	
216			620				625					630					
218	tgg	ggc	ggt	gcc	gag	aat	ctg	gcg	tac	gcc	acg	ctg	gtg	gat	gaa	ggt	2151
219	Trp	Gly	Gly	Ala	Glu	Asn	Leu	Ala	Tyr	Ala	Thr	Leu	Val	Asp	Glu	Gly	
220		635				640						645					
222	att	ccg	gtt	cgc	ctc	tcg	ggt	gaa	gac	tcc	ggt	cgt	gga	acc	ttc	ttc	2199
223	Ile	Pro	Val	Arg	Leu	Ser	Gly	Glu	Asp	Ser	Gly	Arg	Gly	Thr	Phe	Phe	
224	650				655					660					665		
226	cat	cgc	cac	gcg	gtc	gtg	cac	aac	cag	gct	aac	ggt	tca	acc	tat	acg	2247
227	His	Arg	His	Ala	Val	Val	His	Asn	Gln	Ala	Asn	Gly	Ser	Thr	Tyr	Thr	
228				670					675						680		
230	ccg	ctg	cac	cat	att	cat	aac	agc	cag	ggc	gag	ttc	aaa	gtc	tgg	gat	2295
231	Pro	Leu	His	His	Ile	His	Asn	Ser	Gln	Gly	Glu	Phe	Lys	Val	Trp	Asp	
232				685					690					695			
234	tcg	gtg	ctg	tct	gaa	gaa	gcg	gtg	ctg	gcg	ttt	gaa	tac	ggt	tac	gcc	2343
235	Ser	Val	Leu	Ser	Glu	Glu	Ala	Val	Leu	Ala	Phe	Glu	Tyr	Gly	Tyr	Ala	
236		700				705						710					
238	acg	gct	gag	ccg	cgc	gtg	ctg	acc	atc	tgg	gaa	gcg	cag	ttt	ggt	gac	2391
239	Thr	Ala	Glu	Pro	Arg	Val	Leu	Thr	Ile	Trp	Glu	Ala	Glu	Phe	Gly	Asp	
240		715				720				725							
242	ttt	gcc	aac	ggt	gct	cag	gtg	gtg	att	gac	cag	ttc	atc	agc	tct	ggc	2439
243	Phe	Ala	Asn	Gly	Ala	Gln	Val	Val	Ile	Asp	Gln	Phe	Ile	Ser	Ser	Gly	
244	730				735					740					745		
246	gaa	cag	aag	tgg	ggc	cgt	atg	tgt	ggc	ctg	gtg	atg	ttg	ctg	ccg	cat	2487
247	Glu	Gln	Lys	Trp	Gly	Arg	Met	Cys	Gly	Leu	Val	Met	Leu	Leu	Pro	His	
248				750					755					760			
250	ggc	tac	gaa	ggt	cag	gga	ccg	gaa	cac	tcc	tct	gcc	cgt	ctg	gaa	cgc	2535
251	Gly	Tyr	Glu	Gly	Gln	Gly	Pro	Glu	His	Ser	Ser	Ala	Arg	Leu	Glu	Arg	
252			765					770						775			
254	tat	ctg	caa	ctt	tgc	gcc	gag	cag	aac	atg	cag	gtt	tgc	gtc	ccg	tcg	2583
255	Tyr	Leu	Gln	Leu	Cys	Ala	Glu	Gln	Asn	Met	Gln	Val	Cys	Val	Pro	Ser	
256		780				785						790					
258	acg	ccg	gct	cag	gtg	tat	cac	atg	ctg	cgc	cgt	cag	gcg	ctg	cgc	ggg	2631
259	Thr	Pro	Ala	Gln	Val	Tyr	His	Met	Leu	Arg	Arg	Gln	Ala	Leu	Arg	Gly	
260		795				800						805					
262	atg	cgc	cgt	ccg	ctg	gtg	gtg	atg	tcg	ccg	aag	tcg	ctg	tta	cgc	cat	2679
263	Met	Arg	Arg	Pro	Leu	Val	Val	Met	Ser	Pro	Lys	Ser	Leu	Leu	Arg	His	

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264	810		815		820		825		
266	cca	ctg	gcy	atc	tcg	ctg	gat	gaa	ctg
267	Pro	Leu	Ala	Ile	Ser	Ser	Leu	Asp	Glu
268									
270	ccg	gcc	att	ggt	gag	atc	gac	gat	ctg
271	Pro	Ala	Ile	Gly	Glu	Ile	Asp	Asp	Leu
272									
274	gtc	gtg	ctg	tgc	ggc	aag	gtt	tac	tac
275	Val	Val	Leu	Cys	Ser	Gly	Lys	Val	Tyr
276									
278	cgt	aaa	gac	gag	aaa	acc	gat	gtt	gcc
279	Arg	Lys	Asp	Glu	Lys	Thr	Asp	Val	Ala
280									
282	tac	ccg	ttc	ccg	cat	cag	gcg	gta	cag
283	Tyr	Pro	Phe	Pro	His	Gln	Ala	Val	Gln
284	890								
286	cac	gta	cag	gac	ttt	gtc	tgg	tgc	cag
287	His	Val	Gln	Asp	Phe	Val	Trp	Cys	Gln
288									
290	gcc	tgg	tac	tgt	agc	cag	cat	cat	ttc
291	Ala	Trp	Tyr	Cys	Ser	Gln	His	His	Phe
292									
294	gcc	acc	ctg	cgt	tat	gca	ggt	cgc	ccg
295	Ala	Thr	Leu	Arg	Tyr	Ala	Gly	Arg	Pro
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298	ggt	tat	atg	tcc	gta	cac	caa	caa	cag
299	Gly	Tyr	Met	Ser	Val	His	Gln	Gln	Gln
300									
302	gca	ctg	aac	gtc	aat	taa	ttaaaaggaa	agata	atg
303	Ala	Leu	Asn	Val	Asn				
304	970								
306	ctc	gtt	ccc	gac	ctg	cct	gaa	tcg	gtt
307	Leu	Val	Pro	Asp	Leu	Pro	Glu	Ser	Val
308									
310	tgg	cac	aag	aaa	cca	ggc	gat	gca	gtc
311	Trp	His	Lys	Lys	Pro	Gly	Asp	Ala	Val
312									
314	gtc	gaa	att	gaa	act	gac	aaa	gtc	gtg
315	Val	Glu	Ile	Glu	Thr	Asp	Lys	Val	Val
316									
318	gcc	gat	ggc	gtg	ctg	gaa	gcc	gtg	ctg
319	Ala	Asp	Gly	Val	Leu	Glu	Ala	Val	Leu
320									
322	gtt	acg	tcc	cgc	cag	atc	ctg	ggc	cgc
323	Val	Thr	Ser	Arg	Gln	Ile	Leu	Gly	Arg
324									
326	gcg	ggt	aaa	gaa	agc	agt	gcc	aaa	gcg
327	Ala	Gly	Lys	Glu	Ser	Ser	Ala	Lys	Ala
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